

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT: Linsley, Peter S
Ledbetter, Jeffrey A
Damle, Nitin K
10 Brady, William
Wallace, Philip M.

(ii) TITLE OF INVENTION: CTLA4 MOLECULES AND IL4-BINDING
MOLECULES AND USES THEREOF

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(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Merchant & Gould
(B) STREET: 11150 Santa Monica Blvd., Suite 400
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: United States
(F) ZIP: 90025-3395

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
35 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Adriano, Sarah
(B) REGISTRATION NUMBER: 34,470

(C) REFERENCE/DOCKET NUMBER: 9643

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTAGCCACTG AAGCTTCACC ATGGGTGTAC TGCTCACAC

39

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGGCATGGGC TCCTGATCAG GCTTAGAAGG TCCGGGAAA

39

(2) INFORMATION FOR SEQ ID NO:3:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

35 TTTGGGCTCC TGATCAGGAA AATGCTCTTG CTTGGTTGT

39

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAGCAAGAGC ATTTTCCTGA TCAGGAGCCC AAATCTTCTG ACAAAACTCA CACATCCCCA 60
CCGTCCCCAG CACCTGAACT CCTG 84

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTCGACCAG TCTAGAAGCA TCCTCGTGCG ACCGCGAGAG C

41

10 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATTGCACAG TCAAGCTTCC ATGCCCATGG GTTCTCTGGC CACCTTG

47

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCCACAGTG CAGTGATCAT TTGGATCCTG GCATGTGAC

39

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCAGTCTGG TCCTTGCACT CCTGTTTCCA AGCATGGCGA GCATGGCAAT GCACGTGGCC 60
CAGCC 65

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTGGGCTCC TGATCAGAAT CTGGGCACGG TTG

33

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTAGCCACTG AAGCTTCACC AATGGGTGTA CTGCTCACAC AGAGGACGCT GCTCAGTCTG 60
GTCCTTGCAC TC 72

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCAATGCACG TGGCCCAGCC TGCTGTGGTA GTG

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGATGTAACA TGTCTAGATC AATTGATGGG AATAAAATAA GGCTG

45

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..561

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCA ATG CAC GTG GCC CAG CCT GCT GTG GTA CTG GCC AGC AGC CGA GGC 48
Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly
10 1 5 10 15

ATC GCC AGC TTT GTG TGT GAG TAT GCA TCT CCA GGC AAA GCC ACT GAG 96
Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
20 25 30

GTC CGG GTG ACA GTG CTT CGG CAG GCT GAC AGC CAG GTG ACT GAA GTC 144
Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val
35 40 45

TGT GCG GCA ACC TAC ATG ATG GGG AAT GAG TTG ACC TTC CTA GAT GAT 192
Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp
50 55 60

TCC ATC TGC ACG GGC ACC TCC AGT GGA AAT CAA GTG AAC CTC ACT ATC 240
Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
65 70 75 80

CAA GGA CTG AGG GCC ATG GAC ACG GGA CTC TAC ATC TGC AAG GTG GAG 288
Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
85 90 95

CTC ATG TAC CCA CCG CCA TAC TAC CTG GGC ATA GGC AAC GGA ACC CAG 336
Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln
35 100 105 110

ATT TAT GTA ATT GAT CCA GAA CCG TGC CCA GAT TCT GAC TTC CTC CTC 384
 Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Phe Leu Leu
 115 120 125

5 TGG ATC CTT GCA GCA GTT AGT TCG GGG TTG TTT TTT TAT AGC TTT CTC 432
 Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr Ser Phe Leu
 130 135 140

10 CTC ACA GCT GTT TCT TTG AGC AAA ATG CTA AAG AAA AGA AGC CCT CTT 480
 Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg Ser Pro Leu
 145 150 155 160

15 ACA ACA GGG GTC TAT GTG AAA ATG CCC CCA ACA GAG CCA GAA TGT GAA 528
 Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro Glu Cys Glu
 165 170 175

AAG CAA TTT CAG CCT TAT TTT ATT CCC ATC AAT 561
 Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
 180 185

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly

30 1 5 10 15

Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
 20 25 30

35 Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val

	35		40		45											
	Cys	Ala	Ala	Thr	Tyr	Met	Met	Gly	Asn	Glu	Leu	Thr	Phe	Leu	Asp	Asp
	50					55					60					
5	Ser	Ile	Cys	Thr	Gly	Thr	Ser	Ser	Gly	Asn	Gln	Val	Asn	Leu	Thr	Ile
	65					70					75					80
	Gln	Gly	Leu	Arg	Ala	Met	Asp	Thr	Gly	Leu	Tyr	Ile	Cys	Lys	Val	Glu
10					85					90					95	
	Leu	Met	Tyr	Pro	Pro	Pro	Tyr	Tyr	Leu	Gly	Ile	Gly	Asn	Gly	Thr	Gln
				100					105					110		
15	Ile	Tyr	Val	Ile	Asp	Pro	Glu	Pro	Cys	Pro	Asp	Ser	Asp	Phe	Leu	Leu
			115					120					125			
	Trp	Ile	Leu	Ala	Ala	Val	Ser	Ser	Gly	Leu	Phe	Phe	Tyr	Ser	Phe	Leu
	130						135					140				
20	Leu	Thr	Ala	Val	Ser	Leu	Ser	Lys	Met	Leu	Lys	Lys	Arg	Ser	Pro	Leu
	145					150					155					160
	Thr	Thr	Gly	Val	Tyr	Val	Lys	Met	Pro	Pro	Thr	Glu	Pro	Glu	Cys	Glu
25					165				170						175	
	Lys	Gln	Phe	Gln	Pro	Tyr	Phe	Ile	Pro	Ile	Asn					
							180					185				

115
D8